

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 21, 2006, 14:39:05 ; Search time 37.0181 Seconds
 (without alignments)
 938.721 Million cell updates/sec

Title: US-10-539-834-2
 Perfect score: 2135

Sequence: 1 MRCPKCLLCLSLLTLLGLK.....LGPOQAISTRILWQDQPRLQC 397

Scoring table: BLOSUM62

Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep: *
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep: *
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep: *
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep: *
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PECTUS_COMB.pep: *
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 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1595	74.7	389	2	US-09-459-13-13
3	558	26.1	397	3	US-10-019-735-1
4	481	22.5	378	3	US-10-019-735-4
5	467	21.9	378	2	US-09-482-180A-2
6	464	21.8	372	3	US-10-019-735-3
7	459.5	21.5	372	3	US-10-019-735-2
8	379.5	17.8	378	2	US-10-104-047-2503
9	344.5	16.1	422	2	US-09-831-630-10
10	337	15.8	326	2	US-09-055-697-6
11	337	15.8	326	2	US-09-373-902-6
12	322.5	15.1	378	1	US-09-055-697-1
13	322.5	15.1	378	2	US-09-373-902-1
14	322.5	15.1	393	2	US-09-949-016-11567
15	320.5	15.0	378	2	US-09-831-630-13
16	314	14.7	310	2	US-09-831-630-9
17	260	12.2	331	2	US-09-831-630-11
18	260	12.2	331	2	US-09-831-630-12
19	260	12.2	331	2	US-09-891-631-209
20	260	12.2	331	2	US-09-990-444-209
21	260	12.2	331	2	US-09-997-333-209
22	260	12.2	331	2	US-09-992-398-209
23	260	12.2	331	2	US-09-989-735-209
24	260	12.2	331	3	US-09-989-726-209
25	260	12.2	331	3	US-09-997-514-209
26	260	12.2	331	3	US-09-989-728-209

ALIGNMENTS

RESULT 1
 US-09-459-133-2
 Sequence 2, Application US/09459133
 i Patent No. 6416988
 i GENERAL INFORMATION:
 i APPLICANT: Conklin, Darrell C.
 i APPLICANT: Yamamoto, Gayle
 i APPLICANT: Jaspers, Stephen R.
 i APPLICANT: Gao, Zeren
 i TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
 i FILE REFERENCE: 18-77
 i CURRENT APPLICATION NUMBER: US/09-459-133
 i PRIORITY APPLICATION NUMBER: 60/111,697
 i PRIORITY FILING DATE: 1999-12-10
 i NUMBER OF SEQ ID NOS: 20
 i SEQ ID NO: 2
 LENGTH: 397
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i FEATURE:
 i NAME/KEY: VARIANT
 i LOCATION: (137) .. (137)
 i OTHER INFORMATION: Xaa is Gly or Ser
 i FEATURE:
 i NAME/KEY: VARIANT
 i LOCATION: (1) .. (397)
 i OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-459-133-2
 Query Match 99.8%; Score 2131; DB 2; Length 397;
 Best Local Similarity 99.7%; Pred. No. 1.4e-192;
 Matches 336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRCPKCLLCLSLLTLLGLKVIWTSSRLSKAYSPGKSPGTPPTPANPBP7LPANLST 60
 Db 1 MRCPKCLLCLSLLTLLGLKVIWTSSRLSKAYSPGKSPGTPPTPANPBP7LPANLST 60
 QY 61 RLGGTIPPKAYNQQQRNLGSIPGSDSTETGGQAAAT2IPDFASYPDKLRRFL 120
 Db 61 RLGGTIPPKAYNQQQRNLGSIPGSDSTETGGQAAAT2IPDFASYPDKLRRFL 120
 QY 121 SAACRSRSPWQLPGGGGSQVSSCSPTDVPYILLAVKSEPRFAERQAVRTWGSAPGIRL 180
 Db 121 SAACRSRSPWQLPGGGGSQVSSCSPTDVPYILLAVKSEPRFAERQAVRTWGSAPGIRL 180
 QY 181 LFLIGSPGPGAGPQDLSVAWESRYSRSDILLWPLDVPNNOTLKDLLIAGRPHCPTVS 240

RESULT 2
US-10-019-133-13
Sequence 13: Application US/09459133
Patent No. 6416988
GENERAL INFORMATION:
APPLICANT: Yamanoto, Gayle
APPLICANT: Jaspers, Stephen R.
APPLICANT: Conklin, Darrell C.
TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
FILE REFERENCE: 98-77
CURRENT APPLICATION NUMBER: US/09/459,133
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 60/111,697
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 13
LENGTH: 399
TYPE: PRT
ORGANISM: Mus musculus
US-09-459-133-13

Query Match
Best Local Similarity 74.7%; Score 1595; DB 2; Length 389;
Matches 302; Conservative 22; Mismatches 65; Indels 8; Gaps 2;

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Db 1 MRCRKCOLCLSAATLIGKVKYIETWTSRSRSLKAYPSRPTPNAEPLPNTLUSA 58
Qy 61 RUGQTIPFLPAWVQWNRGLSPLPSGSTETGGCQANGAATAEIPDASYKDRLRFLL 120
Db 59 RUGQTGPISSAYVQWQRLGVLPSSTD---CQTGTVASSEILYFQELRFLL 112
Qy 121 SAAACRSFFQWLPGGGSOYSSCSDTDVYLLAVKSEPGFRAEROAVRTGSPAPGIRL 180
Db 113 SAAACRSFFQWLPAGEGSVAQSCSDTDVYLLAVKSEGHFRAOATRTGSPVACTRL 172
Qy 181 LFLLGSPVGEAGPDLDSLVAWESRRYSDLLWDPENQTKDILLIANGRHCPTVS 240
Db 173 LFLLGSPLGMMGGDLSRSLWTSRRYGDLLWDFDPTYNTLKDILLNTLSSHCPDVN 232
Qy 241 FVLLRAQDAFVTPALLAHLRPLPASARSLVLEGEVTOAMPLRKPGFPTVPESEFREGG 300
Db 233 FVLLQVQDDAFTVHPALLEHLLQPTPPTWARSVLYGEITQARPLRKPGFPTVPTFEGD 292
Qy 301 YPAYASGGGYIAGRLLAPWLLAARVAPFPEPDVTVGLCIRALGLVQPAHGFELTAWPA 360
Db 293 YPAYASGGGYISGRLLAPWLLQAARAPFPPDVTGFCPRALGLAPRHPGFLTAWPA 352
Qy 361 DRTADHCAFVNLLVRLPGLPQASIRWKQLODPRLQC 397
Db 353 ERTDPCAVRGFLVHVSQDITWRLHLYVPELQC 389

RESULT 1, Application US/10019735
Patent No. 7005229
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: NO. 7005229e1 Polypeptides
FILE REFERENCE: 11216W01
CURRENT APPLICATION NUMBER: US/10/019,735
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: JP 99/183437
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: JP 2000/74577
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1
LENGTH: 397
TYPE: PRT
ORGANISM: Homo sapiens
US-10-019-735-1

Query Match
Best Local Similarity 26.1%; Score 558; DB 3; Length 397;
Matches 121; Conservative 69; Mismatches 131; Indels 30; Gaps 8;

Qy 69 PEAYWNQQWRIG----SLBGSQDSTETGG----COAWGAANATEPDFAVSP 112
Db 55 PEAYWNREBQKLNRYNPLSMLNTQCEAGRLSNISHLYCSP-DLTVTSVUTGPNLIP 113
Qy 113 KDLRRLPSAACRSFPPWLPGGGSQVSSCDTDVPTVPLAYVSEGRFAEROAVRTW 172
Db 114 DRPKDFDLYLRCRNYSLLI---DQDKCAKX-PFLLAKSLTLPFARRQAIRBSW 166
Qy 173 SPAGP---IRLFLLG-SPGVEAGPDLDSLVAVWESRRYSDLLWDPIDVPPFNQTLKQI 227
Db 167 QESNAGNOTVVRVFLGOTPPDNHPDUSDMKPFESXQDLMWNRTFFNLSLCEVL 226
Qy 228 LIAWLGRHCPTFSVLRQAODDAFVETPALLAHRLPASASRSLVGEVFTQAMPLRKG 287
Db 227 FURWVSTSCPDPTEFVFGDDDFVANTHILNLSKTKADLFGCVTNRGPHDKK 286
Qy 288 GPFYVPPSFEGGPPAYASGGGYIAGRLLAPWLLRAARVAPPFEDVYGLCIRALGLV 347
Db 287 LKYYIPVPPVSYGPPAGGGCFLYSGHILARLYHTDQVHLYPIDDVYGMCLQKGLV 346
Qy 348 PQAHPGFLTAWADRTDH-CAFRNLVLPVPGQASIRLWKLQLODPRLQC 397
Db 347 PEKHKGPFRTFDEEKWONNCSYVDMLVHSRKQPEMIDINSQLQSSHLC 397

RESULT 4
US-10-019-735-4
Sequence 4, Application US/10019735
Patent No. 7005229
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD
TITLE OF INVENTION: NO. 7005229e1 Polypeptides
FILE REFERENCE: 11216W01
CURRENT APPLICATION NUMBER: US/10/019,735
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: JP 99/183437
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: JP 2000/74577
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 4
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-019-735-4

Query Match
Best Local Similarity 22.5%; Score 481; DB 3; Length 378;
US-10-019-735-1

ALIGMENTS						
RESULT 1						
US-09-459-133-2						
; Sequence 2, Application US/09459133						
; Patent No. 6416988						
; GENERAL INFORMATION:						
; APPLICANT: Conklin, Darrell C.						
; APPLICANT: Yamamoto, Gayle						
; APPLICANT: Jaspers, Stephen R.						
; APPLICANT: Gao, Zeren						
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS						
; FILE REFERENCE: 98-77						
; CURRENT APPLICATION NUMBER: US/09/459,133						
; CURRENT FILING DATE: 1999-12-10						
; PRIOR APPLICATION NUMBER: 60/111,697						
; PRIOR FILING DATE: 1998-12-10						
; NUMBER OF SEQ ID NOS: 20						
; SOFTWARE: FastSEQ for Windows Version 3.0						
; SEQ ID NO: 2						
; LENGTH: 397						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
; FEATURE: Any Amino Acid						
; NAME/KEY: VARIANT						
; LOCATION: (137) .. (137)						
; OTHER INFORMATION: Xaa is Gly or Ser						
; FEATURE:						
; NAME/KEY: VARIANT						
; LOCATION: (1) .. (397)						
; OTHER INFORMATION: Xaa = Any Amino Acid						
US-09-459-133-2						
; Query Match 0%						
; Listing first 45 summaries						
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7: /BMC_Celerra_SIDS3/ptodata/2/iaa/backfile1.pep:*						
Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
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2	1474	73.7	389	2	US-09-459-133-13	Sequence 2, Appli
3	558	27.9	397	3	US-10-019-735-1	Sequence 13, Appli
4	4745	23.7	378	3	US-10-019-735-4	Sequence 1, Appli
5	464.5	23.2	372	3	US-10-019-735-3	Sequence 4, Appli
6	460.5	23.0	378	2	US-09-482-1804-2	Sequence 3, Appli
7	459.5	23.0	372	3	US-10-019-735-6	Sequence 2, Appli
8	379.5	19.0	378	2	US-10-014-047-2503	Sequence 2503, Ap
9	344.5	17.2	422	2	US-09-831-630-10	Sequence 10, Appli
10	337	16.9	326	1	US-09-054-097-6	Sequence 1, Appli
11	337	16.9	326	2	US-09-373-902-6	Sequence 6, Appli
12	337	16.9	326	2	US-09-831-630-11	Sequence 11, Appli
13	322.5	16.1	378	1	US-09-057-097-1	Sequence 1, Appli
14	322.5	16.1	378	1	US-09-373-902-1	Sequence 1, Appli
15	322.5	16.1	393	2	US-09-949-016-11567	Sequence 11567, A
16	320.5	16.0	378	2	US-09-831-630-13	Sequence 13, Appli
17	314	15.7	310	2	US-09-831-630-9	Sequence 9, Appli
18	260	13.0	331	2	US-09-831-630-12	Sequence 12, Appli
19	260	13.0	331	2	US-09-997-181-209	Sequence 209, Appli
20	260	13.0	331	2	US-09-990-444-209	Sequence 209, Appli
21	260	13.0	331	2	US-09-997-333-209	Sequence 209, Appli
22	260	13.0	331	2	US-09-998-735-209	Sequence 209, Appli
23	260	13.0	331	2	US-09-985-735-209	Sequence 209, Appli
24	260	13.0	331	3	US-09-989-726-209	Sequence 209, Appli
25	260	13.0	331	3	US-09-999-514-209	Sequence 209, Appli
26	260	13.0	331	3	US-09-999-522-209	Sequence 209, Appli
27	260	13.0	331	3	US-09-997-349-209	Sequence 209, Appli
28	260	13.0	331	3	US-09-989-293A-209	Sequence 209, Appli
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30	250.5	12.9	325	2	US-09-373-902-5	Sequence 5, Appli
31	250.5	12.9	325	2	US-09-373-902-5	Sequence 5, Appli
32	166	8.3	161	2	US-09-270-767-32073	Sequence 47290, A
33	166	8.3	161	2	US-09-270-767-47290	Sequence 45443, A
34	121.5	6.1	472	2	US-09-08-45443	Sequence 3, Appli
35	112.5	5.6	872	1	US-08-491-357-3	Sequence 3, Appli
36	112.5	5.6	872	2	US-08-968-633-3	Sequence 3, Appli
37	112.5	5.6	872	2	US-09-196-466-3	Sequence 3, Appli
38	112.5	5.6	872	2	US-09-669-459A-3	Sequence 3, Appli
39	112.5	5.6	872	5	PCT-US96-108A3-3	Sequence 3, Appli
40	112.5	5.6	3724	1	US-08-804-22C-10	Sequence 4, Appli
41	112.5	5.6	3724	1	US-08-804-198-4	Sequence 2, Appli
42	112	5.6	4472	1	US-08-804-22C-2	Sequence 2, Appli
43	111.5	5.6	1053	2	US-09-902-540-12126	Sequence 12126, A
44	110.5	5.5	636	2	US-09-252-991A-21760	Sequence 21770, A
45	109	5.5	794	2	US-09-252-991A-28569	Sequence 28569, A

Db 206 YSDLMMDFLDVFPENOTIKDILLALWIGRHCPTVSPVLAQDDAPVHTPALLAHRLAPP 265
 Qy 241 ASARSLVYGEVTPQMLPLRKPGPFVTPESFEGGYTPAYASGGYVITAGRLAPWLRAAA 300
 Db 266 ASARSLVYGEVTPQMLPLRKPGPFVTPESFEGGYTPAYASGGYVITAGRLAPWLRAAA 325
 Db 301 RVAPPFFDVTGCLIRALGLVPOAHGFLTAWPDRTAHDCAFRNLLVRLPQASIR 360
 Qy 326 RVAPPFFDVTGCLIRALGLVPOAHGFLTAWPDRTAHDCAFRNLLVRLPQASIR 385
 Db 361 LWKQLODPRLOC 372
 Db 386 LWKQLODPRLOC 397

RESULT 2
 US-09-459-133-13
 Sequence 13, Application US/09459133
 Patent No. 6416988
 GENERAL INFORMATION:
 APPLICANT: Conklin, Darrell C.
 APPLICANT: Yamamoto, Gayle
 APPLICANT: Gao, Zeren
 TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
 CURRENT APPLICATION NUMBER: US/09/459,133
 CURRENT FILING DATE: 1999-12-10
 PRIORITY APPLICATION NUMBER: 60/111,697
 PRIOR FILING DATE: 1998-12-10
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 12
 LENGTH: 369
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-459-133-13

Query Match 73.7%; Score 1474; DB 2; Length 389;
 Best Local Similarity 75.0%; Pred. No. 8.5e-13; Indels 8; Gaps 2;
 Matches 279; Conservative 22; Mismatches 63; Length 389;
 Qy 1 TSSRLSKAYPSRGPPTPSPPTPANPEPTPANLSTRGQTIPFLFAYWNQQQWRLGSLPS 60
 Db 26 TSSRLSKAA-ERGRALISPTPPNAEPTPTNISARLQTGPLSSAYWNQQORQGVLPS 83
 Qy 61 GDSTETGCGQANGAAATIEPDASYPDLDRELLSACRSRSPWLGCGGSQVSSCDT 120
 Db 84 TD-----CQTGTVAASEBILDPBLREFLSSACRSRSPWLGCGGSQVSSCDT 137
 Qy 121 DVPYLLIAVKSEPGFREARQAETWSPAPGIRLILQLSNGEAPDLSLVAVESR 180
 Db 138 DVPYLLIAVKSEPGFHAARQAETWSPVAGTRLLFLGSGPDLISLVTWESR 197
 Qy 181 YSDLMMDFDVFNPQLKDILLALWIGRHCPTVSPVLAQDDAPVHTPALLAHRLAPP 240
 Db 198 YGDLMMDFDVFNPNTKIDILLTWLISHACPDVNFTLQVQDDAFTVPALEHLCOTLPP 257
 Qy 241 ASARSLVYGEVTPQMLPLRKPGPFVTPESFEGGYTPAYASGGYVITAGRLAPWLRAAA 300
 Db 258 TWARSLVYGEITQAKPLRKPGPFVTPKTFEGDTPAYASGGYVITAGRLAPWLRAAA 317
 Qy 301 RVAPPFFDVTGCLIRALGLVPOAHGFLTAWPDRTAHDCAFRNLLVRLPQASIR 360
 Db 318 RVAPPFFDVTGCLIRALGLVPOAHGFLTAWPDRTAHDCAFRNLLVRLPQASIR 377
 Qy 361 LWKQLODPRLOC 372
 Db 378 LWKQLODPRLOC 389

Sequence 1, Application US/10019735
 Patent No. 7005279
 GENERAL INFORMATION:
 APPLICANT: KYOWA HAKKO KOGYO CO., LTD
 TITLE OF INVENTION: No. 7005279ei Polypeptides
 FILE REFERENCE: 11216W01
 CURRENT APPLICATION NUMBER: US/10/019,735
 CURRENT FILING DATE: 2001-12-28
 PRIOR APPLICATION NUMBER: JP 99/183437
 PRIOR FILING DATE: 1999-06-29
 PRIOR APPLICATION NUMBER: JP 2000/74757
 PRIOR FILING DATE: 2000-03-16
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1
 LENGTH: 397
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-019-735-1

Query Match 27.9%; Score 558; DB 3; Length 397;
 Best Local Similarity 34.5%; Pred. No. 5.7e-45;
 Matches 121; Conservative 69; Mismatches 131; Indels 30; Gaps 8;
 Qy 44 PPAWNQOQWRLG-----SLPSGDSPTBTGG-----COAWGAAATAEIPDFAASYP 87
 Db 55 PEAYWNNEOEKLNQYNPILSMLNTQTCBAGRLSNISHLYNCEP-DIRVTSVTFNNLPL 113
 Qy 88 KDLRREFLSAACRSFPOWLPGGGSQVSSCSDTDPYLLAVKSEGRPAEROAVERETWG 147
 Db 114 DRPKDFLLYRCRYNSLLI-----DQDKCARKK-PFLLAITSLPHFARRQAIRESWG 166
 Qy 148 SPAPG---IRIDRLIG-SPVCEAGPDLDSLVAWESERRYSDLLWDFDVPFNQTLKDLL 202
 Db 167 QESNAGNOTQVVRFLGOTPPEDDNHPDLSMNLKFESERKHODILMNYRDTFFPNLSLKEVL 226
 Qy 203 LLAWLGHCHCPTVSPVLAQDDAFAVHPTPALLAHRLAPPASARSLYGEVFTQAMPFLKPG 262
 Db 227 FLRWVSTSCPDTEFPKGDDVFTVNTPHILYLNLSKTRAKDLFIDVIANAGPHRDKE 286
 Qy 263 GPFYVPSFEGGYPAYASGGYVIAGRFLAPWLLRAARAVAPFPEVDYTGICIRALGLV 322
 Db 287 LKYIIPVYVSSGLPPYAGGGFLVPSGHALRLYHTDQVHLYPDPVYTCNLQKGLV 346
 Qy 323 POAHPELTANPADRTADH-CAFRNLLVRLPQGPOSIRLMQQLQPRLQC 372
 Db 347 PEKHKGFRTPDIEKRNKNICSYVDMVHSRKQPMIDWSQLQSAHLKC 397

RESULT 4
 US-10-019-735-4
 Sequence 4, Application US/10019735
 Patent No. 7005279
 GENERAL INFORMATION:
 APPLICANT: KYOWA HAKKO KOGYO CO., LTD
 TITLE OF INVENTION: No. 7005279ei Polypeptides
 FILE REFERENCE: 11216W01
 CURRENT APPLICATION NUMBER: US/10/019,735
 CURRENT FILING DATE: 2001-12-28
 PRIOR APPLICATION NUMBER: JP 99/183437
 PRIOR FILING DATE: 1999-06-29
 PRIOR APPLICATION NUMBER: JP 2000/74757
 PRIOR FILING DATE: 2000-03-16
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 4
 LENGTH: 378
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-019-735-4

Query Match 23.7%; Score 474; DB 3; Length 378;
 Best Local Similarity 39.3%; Pred. No. 5.4e-37;

Copyright GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2006, 14:39:05 ; Search time 26.295 Seconds
(without alignments)
938.721 Million cell updates/sec

Title: US-10-539-834-17
Perfect score: 1508
Sequence: 1 RRFLLSAAACRSFPQWLPGGG.....LGPOQASIRLWKLQLQDRLQC 282

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued_Patents_AH:
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2: /EMC_Celerra_SIDS3_ptodata/2/iaa/6' COMB.pep *
3: /EMC_Celerra_SIDS3_ptodata/2/iaa/7' COMB.pep *
4: /EMC_Celerra_SIDS3_ptodata/2/iaa/8' COMB.pep *
5: /EMC_Celerra_SIDS3_ptodata/2/iaa/9' COMB.pep *
6: /EMC_Celerra_SIDS3_ptodata/2/iaa/10' COMB.pep *
7: /EMC_Celerra_SIDS3_ptodata/2/iaa/backfile1.pep :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1504	99.7	397	2 US-09-459-133-2	Sequence 2, Appli
2	1206	60.0	389	2 US-09-459-133-13	Sequence 1, Appli
3	5265	34.9	397	3 US-10-019-735-1	Sequence 4, Appli
4	4695	31.1	378	3 US-10-019-735-4	Sequence 2, Appli
5	4555	30.2	378	2 US-09-482-180A-2	Sequence 3, Appli
6	4275	28.3	372	3 US-10-019-735-3	Sequence 2, Appli
7	4225	28.0	372	3 US-10-019-735-2	Sequence 2, Appli
8	3795	25.2	378	2 US-09-104-047-2503	Sequence 10, Appli
9	3445	22.8	422	2 US-09-831-330-10	Sequence 6, Appli
10	3377	22.3	326	1 US-09-055-097-6	Sequence 11, Appli
11	3377	22.3	326	2 US-09-793-902-6	Sequence 12, Appli
12	3377	22.3	326	2 US-09-831-630-11	Sequence 1, Appli
13	3222	21.4	378	1 US-09-055-097-1	Sequence 1, Appli
14	3222	21.4	378	2 US-09-73-902-1	Sequence 11, Appli
15	3222	21.4	393	2 US-09-949-016-11567	Sequence 11567, A
16	3220	21.2	378	2 US-09-831-630-13	Sequence 13, Appli
17	3144	20.8	310	2 US-09-131-630-9	Sequence 9, Appli
18	2600	17.2	331	2 US-09-831-630-12	Sequence 209, App
19	2600	17.2	331	2 US-09-991-181-209	Sequence 209, App
20	2600	17.2	331	2 US-09-190-144-209	Sequence 209, App
21	2600	17.2	331	2 US-09-997-133-209	Sequence 209, App
22	2600	17.2	331	2 US-09-992-998-209	Sequence 209, App
23	2600	17.2	331	2 US-09-989-175-209	Sequence 209, App
24	2600	17.2	331	3 US-09-989-126-209	Sequence 209, App
25	2600	17.2	331	3 US-09-997-514-209	Sequence 209, App
26	2600	17.2	331	3 US-09-989-728-209	Sequence 209, App

ALIGNMENTS

RESULT 1
US-09-459-133-2
; Sequence 2, Application US/09459133
; GENERAL INFORMATION:
; Patent No. 6416988
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1, 3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459, 133
; CURRENT FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/111, 697
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (137) .. (137)
; OTHER INFORMATION: Xaa = Gly or Ser
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1) .. (397)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-459-133-2

Query Match 99.7% ; Score 11504 ; DB 2 ; Length 397;
Best Local Similarity 99.6% ; Pred. No. 6.2e-149;
Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRFILFLGSPVGEAGPDLDSLVAVESRYSQVSSCSQCDPVPYLLAVKSEPRGRFAERQAVRETWSGPA 60
Db 116 RRFILFLGSPVGEAGPDLDSLVAVESRYSQVSSCSQCDPVPYLLAVKSEPRGRFAERQAVRETWSGPA 175
QY 61 PGIRFLFLGSPVGEAGPDLDSLVAVESRYSQVSSCSQCDPVPYLLAVKSEPRGRFAERQAVRETWSGPA 120
Db 176 PGIRFLFLGSPVGEAGPDLDSLVAVESRYSQVSSCSQCDPVPYLLAVKSEPRGRFAERQAVRETWSGPA 235
QY 121 CPTVSFLRQDDAFTPHPALLAHRLPPASRSLYLGAEVFTQAMPPLRKPGGPPYVPE 180
Db 236 CPTVSFLRQDDAFTPHPALLAHRLPPASRSLYLGAEVFTQAMPPLRKPGGPPYVPE 295
QY 181 FPEGGYPAYASGGGTYVAGRLAPMLRAARAVAPPFEDVYTGLCIRALGLVPOHPGFL 240

RESULT 2
 Db 296 FPEGGYPAVAGGGVIAVGLAPWNLRAARVAPPFDVYVGLCTRAGVPOAHPGFL 355
 Qy 241 TANPADRTADHCAPFLNLIVRPLGQASIRLWKQLOQDPRLOC 282
 Db 356 TANPADRTADHCAPFLNLIVRPLGQASIRLWKQLOQDPRLOC 397

~~U-09-459-133-13~~
 Sequence 13, Application US/09459133
 ; Patent No. 641698
 ; GENERAL INFORMATION:
 ; APPLICANT: Conklin, Darrell C.
 ; APPLICANT: Yamamoto, Gayle
 ; APPLICANT: Jasper, Stephen R.
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: BETA-1, 3-GALACTOSYLTRANSFERASE HOMOLOGS
 ; FILE REFERENCE: 98-77
 ; CURRENT APPLICATION NUMBER: US/09/459,133
 ; CURRENT FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: 60/111,697
 ; PRIOR FILING DATE: 998-12-10
 ; NUMBER OF SEQ ID: NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 13
 ; LENGTH: 389
 ; TYPE: PRT

TYPE: PRT	ORGANISM: Homo sapiens	US-10-019-735-1	Query Match 34.9%; Score 526.5%; DB 3; Length 397;	Best Local Similarity 37.8%; Pred. No. 1.6e-16;	Matches 108; Conservative 58; Mismatches 107; Indels 13; Gaps 5;
Qy	3 FLLSAACRSFPQMLPGGGSQVSSCSQSDTPVYLLAVKSEPORFABQAVETWGSPAG	62			
Db	119 FLLYLRCRNYSLLI-----DQPDCKAKK--FLLIAKSLTPHEARRQAIRESWQESNA	171			
Qy	63 -----IRLFLLG-SPGEGAGPDLDSLIVAESRRYSPILLWDFDLPVFNENOTLKLILLIAWL	117			
Db	172 GNTVTRVFLGCTPDPDNHPLSDMILKFESEKHDILMNNYRDTPLNLSKEVLLRLRW	231			
Qy	118 GRHCPTVSEVLRQAQDAFVHTPALLAHLRAPPASSRLYLGEVFTQAMPLRKPGSPFVV	177			
Db	232 STSCPDTBFVFKGDDDFVNTNTHILNLYNLSKTKRDLFIGDVTNAGPHRDCKKLKYYI	291			
Qy	178 PESFPFEGGPAYAAGGGYVIGRLAPWLLRAARYAPFPEFDVYTCITRGLVVEQAH	237			
Db	292 PEVTTGSLYPPAGGGFLYSGHLLAIRLYLHTDQVLYPIDDVITGMCLOKGLVIFBKHK	351			
Qy	238 GPLTAVNPADRTADH-CAFRNLLVRLPLGPQASIRLWKLQLODPRLLOC	282			

US-09-459-133-13	Qy	1	RRFLLSAAACRSPPFQWLPGCGSGOVS	Score 1206; DB ² ; Length 389;
	Best Local Similarity	80.0%	SCSDPVDPTILLAYKVSSEPRFAEROAVRETWGSPA	Pred. No. 9.9e-118;
	Matches	78.7%	18; Mismatches	42; Indels 0;
	Matches	222;	Conservative	Gaps 0
	Db	108	RRFLLSAAACRSPPFLWLPAGEGS	Score 1206; DB ² ; Length 389;
	Qy	61	PGIRLFLLGSPVGEAGPDLDSVAYAWESRRYSDLWDFDIDVPEHOTLDLILAWLGRH	Score 1206; DB ² ; Length 389;
	Db	168	AGTRLFLLGSPVGMGGPDLRSLATWESRRYGDLLWDFDIDVPTNLKPGPPYVPE	Score 1206; DB ² ; Length 389;
	Qy	121	GPTVSFVTLRAQDDAFTVTPALLHLRDPASARSLYGEVFTOMPFLRKPGPPYVPE	Score 1206; DB ² ; Length 389;
	Db	228	CPDVNPFLQVQDDAFTVTPALLHLRDPASARSLYGEVFTOMPFLRKPGPPYVPE	Score 1206; DB ² ; Length 389;
US-09-459-133-13	Qy	1	RRFLLSAAACRSPPFQWLPGCGSGOVS	Score 1206; DB ² ; Length 389;
	Best Local Similarity	80.0%	SCSDPVDPTILLAYKVSSEPRFAEROAVRETWGSPA	Pred. No. 9.9e-118;
	Matches	78.7%	18; Mismatches	42; Indels 0;
	Matches	222;	Conservative	Gaps 0
	Db	108	RRFLLSAAACRSPPFLWLPAGEGS	Score 1206; DB ² ; Length 389;
	Qy	61	PGIRLFLLGSPVGEAGPDLDSVAYAWESRRYSDLWDFDIDVPEHOTLDLILAWLGRH	Score 1206; DB ² ; Length 389;
	Db	168	AGTRLFLLGSPVGMGGPDLRSLATWESRRYGDLLWDFDIDVPTNLKPGPPYVPE	Score 1206; DB ² ; Length 389;
	Qy	121	GPTVSFVTLRAQDDAFTVTPALLHLRDPASARSLYGEVFTOMPFLRKPGPPYVPE	Score 1206; DB ² ; Length 389;
	Db	228	CPDVNPFLQVQDDAFTVTPALLHLRDPASARSLYGEVFTOMPFLRKPGPPYVPE	Score 1206; DB ² ; Length 389;

RESULT 4
US-10-019-735-4
; Sequence 4, Application US/10019735
; Patent No. 7005279
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: No. 7005279ei Polypeptides
; FILE REFERENCE: 11216W01
; CURRENT APPLICATION NUMBER: US/10/019,735
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: JPN 99/183437
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: JPN 2000/71757
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0

	Length: 378	Length: 378;
;	TYPE: PRT	
;	ORGANISM: Homo sapiens	
US-10-019-735-4		
Query Match	31.1%	Score 469.5; DB 3;
Best Local Similarity	39.4%	Pred. No. 1.4e-40;
Matches 115; Conservate 38; Mismatches 114; Indels 8		Length 378;
Qy	1	RRFLISAACRSFPQWLPGGGSQVSSCS-DTDVPLYLAVKSEPRGFAERQAVRETWG--
Db	94	RLFLTYRHCNEFSTLL-----BPSGCSKD---PLLAIKSOQHVVEERRAATSTWGRV 144
Qy	58	--SPAGCIGRLFLIGPSYGEAGPDLISLVWESPRYSDILLWDFPDENOTLKLKLLL 114
Db	145	GGWARGRQLKLVFLIG--VAGSAPP--AQLLAYESERFDDILQDFTEDENILKELHLQ 201
Qy	115	AWLGRHCPYTSFVLRQDDDAFVTPALAAHLRLAPASARSLVYGEVFTQAMPLRKEGGP 174
Db	202	RWVVAACPQAHFMKGDDVFVHVNVLBFPLDGDW--AQDLVGVDTQALPNTKVK 259
Qy	175	YYVPPSSPSEG-GYDAYSQGGYNTAGRLPWLRAARVAPPFEDDVTLGLCRALGVP 233
Db	260	YFIPPSMYPATHYPYAGGGYMSRATYVRLQAIMDAELFPPDDYVGMCLRLGSP 319
Qy	234	QAHPGFLT--AWPARDTADHCAFNLILLVPLGPOASIRLWVPLQ 282

RESULT 3

US-10-019-735-1 ; Sequence 1, Application US/10019735
; Patent No. 7005279 ; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: NO. 7005279el Polypeptides
; FILE REFERENCE: 11216N01
; CURRENT APPLICATION NUMBER: US/10/019,735
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: JP 99/183437
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: JP 20000/74757
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 397

Qy 181 FPEGGPAYASGGYVAGRLAWLRLAARVAPPFEDVYTGICIRAGLVPORHPGFL 240
; Db 288 FPEGDPAYASGGYVTSGRILAFWLLQAAARVAPPFEDVYTGICIRAGLVPORHPGFL 347

Qy 241 TAWPAERTADRCFARNLILVRLPQGPQASTRLWKLQDPELQ 282
; Db 348 TAWPAERTDPCAVRGLLVLHPVSPQDTIWLWHLWVPELQ 389